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AGATGGAGTT TTGCCATGTT GGCCAGGCTG ATCATGAACT CCTGGCCTCA   40750
AGTGATCTGC CTGCCTCAGC CTCCCAAAGT GCTGGGATTA CAGGTGTGAA   40800
CCACTGTGCT CGGCCTAATC TTACAAGTTT TCAATATTTA AAGAGTGCTA   40850
ACTTTGTTGA CAATATAAAA CATATTTGAG AAAAAGAGAT ATAAGCATCT   40900
TATTTAGAAT TATGAAAATA TCAATAGACC TACAGCCCAC TAAAGCTTTT   40950
CTTCATAAGC TCTTGCCTAT ATTGATTCGC TCCTGTGAAT ATGCATTAAT   41000
TTGATTTAAA TAATAAGTAT GTATAAGAAA TAACACTTTT CCTTAATTTT   41050
TAAGAACGTT CAACAGTTTT TAATTTGAAT TCCAATAGTG AAATACATAG   41100
AAAATATAAA ATTTTCTGTA GTTTAGCCAA ATTGTTTTTG TTTCACCACA   41150
GCATTCTACC AAAATTTCTT AATAACAGTA AGAAAATGAA TGCATACCTC   41200
CTGCAGGGAG AGGGGAGTTA GGCAGTTTAT GGGCATAGTT ACAAGTGAGA   41250
AATTTCATTG GCTACCATTT ACGCTAAATT CATAAAAACT GCATTCAATT   41300
CTATATATCT ATTTTCTTTA CATAAAAAAG GTTTCAATTA TTGGCCATTA   41350
AATAAAATAG CCACCATTCC AGAAGTTGTG TCATGTTTAT CCTTTTTATA   41400
CCACCATCAT ATTGCCTATT ATATAGATTG TGTGTGTTCC ATTTTCTGTA   41450
ATGGGCCAGA CAGTAAGTAT TTCTGGCTTT GGAGTCCATA TGGTCTCTAT   41500
CATAACTACT CATCTCTGCC ATTGTAGCTT AAAGATTATC TAGGTCAAAT   41550
GCCTAAGTGA TATAGTGTTG AAATACAAGT TATATAATAT AGGCTGCCAC   41600
AAAAAAAAAT TTATTTGGTC TAAAAAAGAT TTCATGACTT TTGTAGCAGC   41650
ATGGGTGGGG CATGCACCAC TTGGTTAACT CGGTGTATCT TTCTCCTTTG   41700
CAGATCTGTC CAACTCAATG GTCTAACTCT AAAGATGGTG GATGATCAAA   41750
CCTTGCCACC TTTAATGGAA AAACCTCTCC GGCCAGGGAG TTCACTGGGC   41800
TTGCCAGCTT TCTCATATAG TTTTTTTGTG ATAAGAAATG CCAAAGTTGC   41850
TGCTTGCATC TGAAAATAAA ATATACTAGT CCTGACACTG AATTTTTCAA   41900
GTATACTAAG AGTAAAGCAA CTCAAGTTAT AGGAAAGGAA GCAGATACCT   41950
TGCAAAGCAA CTAGTGGGTG CTTGAGAGAC ACTGGGACAC TGTCAGTGCT   42000
AGATTTAGCA CAGTATTTTG ATCTCGCTAG GTAGAACACT GCTAATAATA   42050
ATAGCTAATA ATACCTTGTT CCAAATACTG CTTAGCATTT TGCATGTTTT   42100
ACTTTTATCT AAAGTTTTGT TTTGTTTTAT TATTTATTTA TTTATTTATT   42150
TTGAGACAGA ATCTCTCTCT GTCACCCAGG CTGGAGTGCC ATGGTGCGAT   42200
CTTGGCTCAC TGCAACTTTA AGCAATTCTC CTGCCTCAGC TTCCTGAGTA   42250
GCTGGGATTA TAGGCGTGTG CCACCACGCC CAGCTACTTT CTATATTTTT   42300
TGTAGAGATG GAGTTTCGCC ATATTGGCCA AGCTGGTCTC GAACTCCTGT   42350
CCTCGAACTC CTGTCCTCAA GTGATCCACC CGCCTCAGCC TCTCAAAGTG   42400
CTGGGATTAC AGGTGTGAGC CACCACACCC AGCAGTGTTT TATTTTTGAG   42450
ACAGGGTATC ATTCTGTTGC CCAGGCTTGA GTGCAGTGGT GCAATCATAG   42500
ATCACTGCAG CCTTTTAACT CCTGGGCTCA AGTCATCCTC CTGCTTAGCC   42550
TCCCAAGTAG CTAGGACCAC AGACACATGC CATCACACTT GGCTATTTTT   42600
AAAAAATTTT TTGTAGAGAT GGGGTCTCGC TATGTTACCC AAACTGGTCC   42650
TGAACTCCTG GACTCAATTG ATCCTCCCAC CTTGGCCTTC CAGGTGCTGG   42700
GATTTCTTTG GGAGTACAGC ATGGTACAGC AGGAGATCAT TTGATGTTAC   42750
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CTCTGTGCAG TGTTGCTAGT CAGCGAAAGA CTATAATACC TGTGGGGACA    42800
GCGATTAGCC ACCACAACCA GTCTTTATTT AAAGTTATTA AAAATGGCTG    42850
GGCGCAGTGG CTCACACCTG TAATCCTAGC ACTTTGGGAG GCCGAGGCAG    42900
ATGGATCACC TGACGTGAGG AATTTGAGAC CAGCCTGGCC AACATGGTGA    42950
AACCCCATCT CTACTAAAAA ATACAAAAAT TAGCTGGGTG TGGTCCTGTA    43000
GTCCCAGCTA CTTGGGAGGC TGGGGCAGGA GAATTACTTG AACCCAGGAG    43050
GCAGAGGTTG CAGTGAGCCG AGATTGTGCC ACTGCACTCC AGCCTGGGTG    43100
ACAGAGAGAG ATTCCATCTC AAAAAAACAA GTTATTAAAA ATGTATATGA    43150
ATGCTCCTAA TATGGTCAGG AAGCAAGGAA GCGAAGGATA TATTATGAGT    43200
TTTAAGAAGG TGCTTAGCTG TATATTTATC TTTCAAAATG TATTAGAAGA    43250
TTTTAGAATT CTTTCCTTCA TGTGCCATCT CTACAGGCAC CCATCAGAAA    43300
AAGCATACTG CCGTTACCGT GAAACTGGTT GTAAAAGAGA AACTATCTAT    43350
TTGCACCTTA AAAGACAGCT AGATTTTGCT GATTTTCTTC TTTCGGTTTT    43400
CTTTGTCAGC AATAATATGT GAGAGGACAG ATTGTTAGAT ATGATAGTAT    43450
AAAAAATGGT TAATGACAAT TCAGAGGCGA GGAGATTCTG TAAACTTAAA    43500
ATTACTATAA ATGAAATTGA TTTGTCAAGA GGATAAATTT TAGAAAACAC    43550
CCAATACCTT ATAACTGTCT GTTAATGCTT GCTTTTTCTC TACCTTTCTT    43600
CCTTGTTTCA GTTGGGAAGC TTTTGGCTGC AAGTAACAGA AACTCCTAAT    43650
TCAAATGGCT TAAGCAATAA GGAAATGTAT ATTCCCACAT AACTAGACGT    43700
TCAAACAGGC CAGGCTCCAG CACTTCAGTA CGTCACCAGG GATCTGGGTT    43750
CTTCCCAGCT CTCTGCTCTG CCATCTTTAG CGCTGGCTTC ATTCTCAGAC    43800
TCTGGTAGCA TGATGGCTGT AGCTGTTTCA TGGGCCCCTT CAAACCTCAT    43850
AGCAACCAGA GGAAGAAAAT GAGCCATTTT TTGAGTCTCC TTCATAGACT    43900
TGAATAACTC TTTTTCAGAG CTTCTCACAG CAAACCTCTC CTCATGTCTC    43950
CTCATGTCTT ATTGTTCAGA AATGGGTAAT GTGGCCATTT CACCAGTCAC    44000
TGCCAACAAC AACGAGGTTC CTATAATTGT CTCTGAGTAA CCCTTTGGAA    44050
TGGAGAGGGT GTTGGTCAGT CTACAAACTG AACACTGCAG TTCTGCGCTT    44100
TTTACCAGTG AAAAAATGTA ATTATTTTCC CCTCTTAAGG ATTAATATTC    44150
TTCAAATGTA TGCCTGTTAT GGATATAGTA TCTTTAAAAT TTTTTATTTT    44200
AATAGCTTTA GGGGTACACA CTTTTTGCTT ACAGGGGTGA ATTGTGTAGT    44250
GGTGAAGACT CGGCTTTTAA TGTACTTGTC ACCTGAGTGA TGTACATTGT    44300
ACCCAATAGG TAATTTTTCA TCCATTACCC TCCTTCCGCC CTCTTCCCTT    44350
CTGAGTCTCC AACATCCCTT ATACCACTGT GTATGTTCTT GTGTACCTAC    44400
AGCTAAGCTT CCACTTATAA GTGAGAACAT GCAGTATTTG GTTTTCCATT    44450
CCTGAGTTAC TTCCCTTAGG ATAACAGCCC CCAGTTCCGT CCAAGTTGCT    44500
GCAAAATACA TTATTCTTCT TTATGGCTGA GTAATAGTCC ATGGTACATA    44550
TATACCACAT TTTCTTTATC CACTTATCAG TTGATGGACA CTTAGGTTAA    44600
TTCCATTCAA TTTCATTCAA TTTAAGTATA TTTGTAAGGA GCTAAAGCTG    44650
AAAATTAAAT TTTAGATCTT TCAATACTCT TAAATTTTAT ATGTAAGTGG    44700
TTTTTATATT TTCACATTTG AAATAAAGTA ATTTTTATAA CCTTGATATT    44750
GTATGACTAT TCTTTTAGTA ATGTAAAGCC TACAGACTCC TACATTTGGA    44800
ACCACTAGTG TGTTGTTTCA CCCCTTGTTA TACTATCAGG ATCCTCGA     44848
```

(2)   INFORMATION FOR SEQ ID NO:43:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 2396

        (B)   TYPE: nucleic acid

        (C)   STRANDEDNESS: double

        (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:43

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TTTCTAGTTG CTTTTAGCCA ATGTCGGATC AGGTTTTTCA AGCGACAAAG     50
AGATACTGAG ATCCTGGGCA GAGGACATCC TAGCTCGGTC AGATTTGGGC    100
AGGCTCAAGT GACCAGTGTC TTAAGGCAGA AGGGAGTCGG GGTAGGGTCT    150
GGCTGAACCC TCAACCGGGG CTTTTAACTC AGGGTCTAGT CCTGGCGCCA    200
AATGGATGGG ACCTAGAAAA GGTGACAGAG TGCGCAGGAC ACCAGGAAGC    250
TGGTCCCACC CCTGCGCGGC TCCCGGGCGC TCCCTCCCCA GGCCTCCGAG    300
GATCTTGGAT TCTGGCCACC TCCGCACCCT TTGGATGGGT GTGGATGATT    350
TCAAAAGTGG ACGTGACCGC GGCGGAGGGG AAAGCCAGCA CGGAAATGAA    400
AGAGAGCGAG GAGGGGAGGG CGGGGAGGGG AGGGCGCTAG GGAGGGACTC    450
CCGGGAGGGG TGGGAGGGAT GGAGCGCTGT GGGAGGGTAC TGAGTCCTGG    500
CGCCAGAGGC GAAGCAGGAC CGGTTGCAGG GGGCTTGAGC CAGCGCGCCG    550
GCTGCCCCAG CTCTCCCGGC AGCGGGCGGT CCAGCCAGGT GGGATGCTGA    600
GGCTGCTGCT GCTGTGGCTC TGGGGGCCGC TCGGTGCCCT GGCCCAGGGC    650
GCCCCCGCGG GGACCGCGCC GACCGACGAC GTGGTAGACT TGGAGTTTTA    700
CACCAAGCGG CCGCTCCGAA GCGTGAGTCC CTCGTTCCTG TCCATCACCA    750
TCGACGCCAG CCTGGCCACC GACCCGCGCT TCCTCACCTT CCTGGGCTCT    800
CCAAGGCTCC GTGCTCTGGC TAGAGGCTTA TCTCCTGCAT ACTTGAGATT    850
TGGCGGCACA AAGACTGACT TCCTTATTTT TGATCCGGAC AAGGAACCGA    900
CTTCCGAAGA AAGAAGTTAC TGGAAATCTC AAGTCAACCA TGATATTTGC    950
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AGGTCTGAGC CGGTCTCTGC TGCGGTGTTG AGGAAACTCC AGGTGGAATG    1000
GCCCTTCCAG GAGCTGTTGC TGCTCCGAGA GCAGTACCAA AAGGAGTTCA    1050
AGAACAGCAC CTACTCAAGA AGCTCAGTGG ACATGCTCTA CAGTTTTGCC    1100
AAGTGCTCGG GGTTAGACCT GATCTTTGGT CTAAATGCGT TACTACGAAC    1150
CCCAGACTTA CGGTGGAACA GcTCCAACGC CCAGCTTCTC CTTGACTACT    1200
GCTCTTCCAA GGGTTATAAC ATcTCCTGGG AACTGGGCAA TGAGCCCAAC    1250
AGTTTcTGGA AGAAAGCTCA CATTCTCATC GATGGGTTGC AGTTAGGAGA    1300
AGACTTTGTG GAGTTGCATA AACTTcTACA AAGGTCAGCT TTCCAAAATG    1350
CAAAACTCTA TGGTCCTGAC ATCGGTCAGC CTCGAGGGAA GACAGTTAAA    1400
CTGCTGAGGA GTTTCCTGAA GGCTGGCGGA GAAGTGATCG ACTCTCTTAC    1450
ATGGCATCAC TATTACTTGA ATGGACGCAT CGCTACCAAA GAAGATTTTC    1500
TGAGCTCTGA TGCGCTGGAC ACTTTTATTC TCTCTGTGCA AAAAATTCTG    1550
AAGGTCACTA AAGAGATCAC ACCTGGCAAG AAGGTCTGGT TGGGAGAGAC    1600
GAGCTCAGCT TACGGTGGCG GTGCACCCTT GCTGTCCAAC ACCTTTGCAG    1650
CTGGCTTTAT GTGGCTGGAT AAATTGGGCC TGTCAGCCCA GATGGGCATA    1700
GAAGTCGTGA TGAGGCAGGT GTTCTTCGGA GCAGGCAACT ACCACTTAGT    1750
GGATGAAAAC TTTGAGCCTT TACCTGATTA CTGGCTCTCT CTTCTGTTCA    1800
AGAAACTGGT AGGTCCCAGG GTGTTACTGT CAAGAGTGAA AGGCCCAGAC    1850
AGGAGCAAAC TCCGAGTGTA TCTCCACTGC ACTAACGTCT ATCACCCACG    1900
ATATCAGGAA GGAGATCTAA CTCTGTATGT CCTGAACCTC CATAATGTCA    1950
CCAAGCACTT GAAGGTACCG CCTCCGTTGT TCAGGAAACC AGTGGATACG    2000
TACCTTCTGA AGCCTTCGGG GCCGGATGGA TTACTTTCCA AATCTGTCCA    2050
ACTGAACGGT CAAATTCTGA AGATGGTGGA TGAGCAGACC CTGCCAGCTT    2100
TGACAGAAAA ACCTCTCCCC GCAGGAAGTG CACTAAGCCT GCCTGCCTTT    2150
TCCTATGGTT TTTTTGTCAT AAGAAATGCC AAAATCGCTG CTTGTATATG    2200
AAAATAAAAG GCATACGGTA CCCCTGAGAC AAAAGCCGAG GGGGGTGTTA    2250
TTCATAAAAC AAAACCCTAG TTTAGGAGGC CACCTCCTTG CCGAGTTCCA    2300
GAGCTTCGGG AGGGTGGGGT ACACTTCAGT ATTACATTCA GTGTGGTGTT    2350
CTCTCTAAGA AGAATACTGC AGGTGGTGAC AGTTAATAGC ACTGTG       2396
```

(2)   INFORMATION FOR SEQ ID NO:44:
         (i)   SEQUENCE CHARACTERISTICS:
                  (A)   LENGTH: 535
                  (B)   TYPE: amino acid
                  (C)   STRANDEDNESS: single
                  (D)   TOPOLOGY: linear
         (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:44

```
Met Leu Arg Leu Leu Leu Leu Trp Leu Trp Gly Pro Leu Gly Ala
              5                  10                  15
Leu Ala Gln Gly Ala Pro Ala Gly Thr Ala Pro Thr Asp Asp Val
              20                 25                  30
Val Asp Leu Glu Phe Tyr Thr Lys Arg Pro Leu Arg Ser Val Ser
              35                 40                  45
Pro Ser Phe Leu Ser Ile Thr Ile Asp Ala Ser Leu Ala Thr Asp
              50                 55                  60
Pro Arg Phe Leu Thr Phe Leu Gly Ser Pro Arg Leu Arg Ala Leu
              65                 70                  75
Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly Thr Lys
              80                 85                  90
Thr Asp Phe Leu Ile Phe Asp Pro Asp Lys Glu Pro Thr Ser Glu
              95                 100                 105
Glu Arg Ser Tyr Trp Lys Ser Gln Val Asn His Asp Ile Cys Arg
              110                115                 120
Ser Glu Pro Val Ser Ala Ala Val Leu Arg Lys Leu Gln Val Glu
              125                130                 135
Trp Pro Phe Gln Glu Leu Leu Leu Leu Arg Glu Gln Tyr Gln Lys
              140                145                 150
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Glu Phe Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Met Leu
            155             160             165
Tyr Ser Phe Ala Lys Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu
            170             175             180
Asn Ala Leu Leu Arg Thr Pro Asp Leu Arg Trp Asn Ser Ser Asn
            185             190             195
Ala Gln Leu Leu Leu Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile
            200             205             210
Ser Trp Glu Leu Gly Asn Glu Pro Asn Ser Phe Trp Lys Lys Ala
            215             220             225
His Ile Leu Ile Asp Gly Leu Gln Leu Gly Glu Asp Phe Val Glu
            230             235             240
Leu His Lys Leu Leu Gln Arg Ser Ala Phe Gln Asn Ala Lys Leu
            245             250             255
Tyr Gly Pro Asp Ile Gly Gln Pro Arg Gly Lys Thr Val Lys Leu
            260             265             270
Leu Arg Ser Phe Leu Lys Ala Gly Gly Glu Val Ile Asp Ser Leu
            275             280             285
Thr Trp His His Tyr Tyr Leu Asn Gly Arg Ile Ala Thr Lys Glu
            290             295             300
Asp Phe Leu Ser Ser Asp Ala Leu Asp Thr Phe Ile Leu Ser Val
            305             310             315
Gln Lys Ile Leu Lys Val Thr Lys Glu Ile Thr Pro Gly Lys Lys
            320             325             330
Val Trp Leu Gly Glu Thr Ser Ser Ala Tyr Gly Gly Gly Ala Pro
            335             340             345
Leu Leu Ser Asn Thr Phe Ala Ala Gly Phe Met Trp Leu Asp Lys
            350             355             360
Leu Gly Leu Ser Ala Gln Met Gly Ile Glu Val Val Met Arg Gln
            365             370             375
Val Phe Phe Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe
            380             385             390
Glu Pro Leu Pro Asp Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu
            395             400             405
Val Gly Pro Arg Val Leu Leu Ser Arg Val Lys Gly Pro Asp Arg
            410             415             420
Ser Lys Leu Arg Val Tyr Leu His Cys Thr Asn Val Tyr His Pro
            425             430             435
Arg Tyr Gln Glu Gly Asp Leu Thr Leu Tyr Val Leu Asn Leu His
            440             445             450
Asn Val Thr Lys His Leu Lys Val Pro Pro Pro Leu Phe Arg Lys
            455             460             465
Pro Val Asp Thr Tyr Leu Leu Lys Pro Ser Gly Pro Asp Gly Leu
            470             475             480
Leu Ser Lys Ser Val Gln Leu Asn Gly Gln Ile Leu Lys Met Val
            485             490             495
Asp Glu Gln Thr Leu Pro Ala Leu Thr Glu Lys Pro Leu Pro Ala
            500             505             510
Gly Ser Ala Leu Ser Leu Pro Ala Phe Ser Tyr Gly Phe Phe Val
            515             520             525
Ile Arg Asn Ala Lys Ile Ala Ala Cys Ile
            530             535
```

(2)   INFORMATION FOR SEQ ID NO:45:

　　　(i)   SEQUENCE CHARACTERISTICS:

　　　　　　(A)   LENGTH: 2396

　　　　　　(B)   TYPE: nucleic acid

(C)   STRANDEDNESS: double
(D)   TOPOLOGY: linear
(xi)   SEQUENCE DESCRIPTION: SEQ ID NO:45

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                                          TT TCT AGT      8
TGC TTT TAG CCA ATG TCG GAT CAG GTT TTT CAA GCG ACA AAG AGA    53
TAC TGA GAT CCT GGG CAG AGG ACA TCC TAG CTC GGT CAG ATT TGG    98
GCA GGC TCA AGT GAC CAG TGT CTT AAG GCA GAA GGG AGT CGG GGT   143
AGG GTC TGG CTG AAC CCT CAA CCG GGG CTT TTA ACT CAG GGT CTA   188
GTC CTG GCG CCA AAT GGA TGG GAC CTA GAA AAG GTG ACA GAG TGC   233
GCA GGA CAC CAG GAA GCT GGT CCC ACC CCT GCG CGG CTC CCG GGC   278
GCT CCC TCC CCA GGC CTC CGA GGA TCT TGG ATT CTG GCC ACC TCC   323
GCA CCC TTT GGA TGG GTG TGG ATG ATT TCA AAA GTG GAC GTG ACC   368
GCG GCG GAG GGG AAA GCC AGC ACG GAA ATG AAA GAG AGC GAG GAG   413
GGG AGG GCG GGG AGG GGA GGG CGC TAG GGA GGG ACT CCC GGG AGG   458
GGT GGG AGG GAT GGA GCG CTG TGG GAG GGT ACT GAG TCC TGG CGC   503
CAG AGG CGA AGC AGG ACC GGT TGC AGG GGG CTT GAG CCA GCG CGC   548
CGG CTG CCC CAG CTC TCC CGG CAG CGG GCG GTC CAG CCA GGT GGG   593
ATG CTG AGG CTG CTG CTG CTG TGG CTC TGG GGG CCG CTC GGT GCC   638
Met Leu Arg Leu Leu Leu Leu Trp Leu Trp Gly Pro Leu Gly Ala
          5                   10                  15


CTG GCC CAG GGC GCC CCC GCG GGG ACC GCG CCG ACC GAC GAC GTG   683
Leu Ala Gln Gly Ala Pro Ala Gly Thr Ala Pro Thr Asp Asp Val
          20                  25                  30


GTA GAC TTG GAG TTT TAC ACC AAG CGG CCG CTC CGA AGC GTG AGT   728
Val Asp Leu Glu Phe Tyr Thr Lys Arg Pro Leu Arg Ser Val Ser
          35                  40                  45


CCC TCG TTC CTG TCC ATC ACC ATC GAC GCC AGC CTG GCC ACC GAC   773
Pro Ser Phe Leu Ser Ile Thr Ile Asp Ala Ser Leu Ala Thr Asp
          50                  55                  60


CCG CGC TTC CTC ACC TTC CTG GGC TCT CCA AGG CTC CGT GCT CTG   818
Pro Arg Phe Leu Thr Phe Leu Gly Ser Pro Arg Leu Arg Ala Leu
          65                  70                  75


GCT AGA GGC TTA TCT CCT GCA TAC TTG AGA TTT GGC GGC ACA AAG   863
Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly Thr Lys
          80                  85                  90


ACT GAC TTC CTT ATT TTT GAT CCG GAC AAG GAA CCG ACT TCC GAA   908
Thr Asp Phe Leu Ile Phe Asp Pro Asp Lys Glu Pro Thr Ser Glu
          95                  100                 105


GAA AGA AGT TAC TGG AAA TCT CAA GTC AAC CAT GAT ATT TGC AGG   953
Glu Arg Ser Tyr Trp Lys Ser Gln Val Asn His Asp Ile Cys Arg
          110                 115                 120


TCT GAG CCG GTC TCT GCT GCG GTG TTG AGG AAA CTC CAG GTG GAA   998
Ser Glu Pro Val Ser Ala Ala Val Leu Arg Lys Leu Gln Val Glu
          125                 130                 135


TGG CCC TTC CAG GAG CTG TTG CTG CTC CGA GAG CAG TAC CAA AAG  1043
Trp Pro Phe Gln Glu Leu Leu Leu Leu Arg Glu Gln Tyr Gln Lys
          140                 145                 150
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GAG TTC AAG AAC AGC ACC TAC TCA AGA AGC TCA GTG GAC ATG CTC      1088
Glu Phe Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Met Leu
            155                 160                 165


TAC AGT TTT GCC AAG TGC TCG GGG TTA GAC CTG ATC TTT GGT CTA      1133
Tyr Ser Phe Ala Lys Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu
            170                 175                 180


AAT GCG TTA CTA CGA ACC CCA GAC TTA CGG TGG AAC AGc TCC AAC      1178
Asn Ala Leu Leu Arg Thr Pro Asp Leu Arg Trp Asn Ser Ser Asn
            185                 190                 195


GCC CAG CTT CTC CTT GAC TAC TGC TCT TCC AAG GGT TAT AAC ATc      1223
Ala Gln Leu Leu Leu Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile
            200                 205                 210


TCC TGG GAA CTG GGC AAT GAG CCC AAC AGT TTc TGG AAG AAA GCT      1268
Ser Trp Glu Leu Gly Asn Glu Pro Asn Ser Phe Trp Lys Lys Ala
            215                 220                 225


CAC ATT CTC ATC GAT GGG TTG CAG TTA GGA GAA GAC TTT GTG GAG      1313
His Ile Leu Ile Asp Gly Leu Gln Leu Gly Glu Asp Phe Val Glu
            230                 235                 240


TTG CAT AAA CTT cTA CAA AGG TCA GCT TTC CAA AAT GCA AAA CTC      1358
Leu His Lys Leu Leu Gln Arg Ser Ala Phe Gln Asn Ala Lys Leu
            245                 250                 255


TAT GGT CCT GAC ATC GGT CAG CCT CGA GGG AAG ACA GTT AAA CTG      1403
Tyr Gly Pro Asp Ile Gly Gln Pro Arg Gly Lys Thr Val Lys Leu
            260                 265                 270


CTG AGG AGT TTC CTG AAG GCT GGC GGA GAA GTG ATC GAC TCT CTT      1448
Leu Arg Ser Phe Leu Lys Ala Gly Gly Glu Val Ile Asp Ser Leu
            275                 280                 285


ACA TGG CAT CAC TAT TAC TTG AAT GGA CGC ATC GCT ACC AAA GAA      1493
Thr Trp His His Tyr Tyr Leu Asn Gly Arg Ile Ala Thr Lys Glu
            290                 295                 300


GAT TTT CTG AGC TCT GAT GCG CTG GAC ACT TTT ATT CTC TCT GTG      1538
Asp Phe Leu Ser Ser Asp Ala Leu Asp Thr Phe Ile Leu Ser Val
            305                 310                 315


CAA AAA ATT CTG AAG GTC ACT AAA GAG ATC ACA CCT GGC AAG AAG      1583
Gln Lys Ile Leu Lys Val Thr Lys Glu Ile Thr Pro Gly Lys Lys
            320                 325                 330


GTC TGG TTG GGA GAG ACG AGC TCA GCT TAC GGT GGC GGT GCA CCC      1628
Val Trp Leu Gly Glu Thr Ser Ser Ala Tyr Gly Gly Gly Ala Pro
            335                 340                 345


TTG CTG TCC AAC ACC TTT GCA GCT GGC TTT ATG TGG CTG GAT AAA      1673
Leu Leu Ser Asn Thr Phe Ala Ala Gly Phe Met Trp Leu Asp Lys
            350                 355                 360
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TTG GGC CTG TCA GCC CAG ATG GGC ATA GAA GTC GTG ATG AGG CAG      1718
Leu Gly Leu Ser Ala Gln Met Gly Ile Glu Val Val Met Arg Gln
                365             370             375

GTG TTC TTC GGA GCA GGC AAC TAC CAC TTA GTG GAT GAA AAC TTT      1763
Val Phe Phe Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe
                380             385             390

GAG CCT TTA CCT GAT TAC TGG CTC TCT CTT CTG TTC AAG AAA CTG      1808
Glu Pro Leu Pro Asp Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu
                395             400             405

GTA GGT CCC AGG GTG TTA CTG TCA AGA GTG AAA GGC CCA GAC AGG      1853
Val Gly Pro Arg Val Leu Leu Ser Arg Val Lys Gly Pro Asp Arg
                410             415             420

AGC AAA CTC CGA GTG TAT CTC CAC TGC ACT AAC GTC TAT CAC CCA      1898
Ser Lys Leu Arg Val Tyr Leu His Cys Thr Asn Val Tyr His Pro
                425             430             435

CGA TAT CAG GAA GGA GAT CTA ACT CTG TAT GTC CTG AAC CTC CAT      1943
Arg Tyr Gln Glu Gly Asp Leu Thr Leu Tyr Val Leu Asn Leu His
                440             445             450

AAT GTC ACC AAG CAC TTG AAG GTA CCG CCT CCG TTG TTC AGG AAA      1988
Asn Val Thr Lys His Leu Lys Val Pro Pro Pro Leu Phe Arg Lys
                455             460             465

CCA GTG GAT ACG TAC CTT CTG AAG CCT TCG GGG CCG GAT GGA TTA      2033
Pro Val Asp Thr Tyr Leu Leu Lys Pro Ser Gly Pro Asp Gly Leu
                470             475             480

CTT TCC AAA TCT GTC CAA CTG AAC GGT CAA ATT CTG AAG ATG GTG      2078
Leu Ser Lys Ser Val Gln Leu Asn Gly Gln Ile Leu Lys Met Val
                485             490             495

GAT GAG CAG ACC CTG CCA GCT TTG ACA GAA AAA CCT CTC CCC GCA      2123
Asp Glu Gln Thr Leu Pro Ala Leu Thr Glu Lys Pro Leu Pro Ala
                500             505             510

GGA AGT GCA CTA AGC CTG CCT GCC TTT TCC TAT GGT TTT TTT GTC      2168
Gly Ser Ala Leu Ser Leu Pro Ala Phe Ser Tyr Gly Phe Phe Val
                515             520             525

ATA AGA AAT GCC AAA ATC GCT GCT TGT ATA TGA AAA TAA AAG GCA      2213
Ile Arg Asn Ala Lys Ile Ala Ala Cys Ile
                530             535

TAC GGT ACC CCT GAG ACA AAA GCC GAG GGG GGT GTT ATT CAT AAA      2258
ACA AAA CCC TAG TTT AGG AGG CCA CCT CCT TGC CGA GTT CCA GAG      2303
CTT CGG GAG GGT GGG GTA CAC TTC AGT ATT ACA TTC AGT GTG GTG      2348
TTC TCT CTA AGA AGA ATA CTG CAG GTG GTG ACA GTT AAT AGC ACT      2393
GTG                                                              2396
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(2)   INFORMATION FOR SEQ ID NO:46:
       (i)   SEQUENCE CHARACTERISTICS:
              (A)   LENGTH: 385

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          (B)     TYPE:           nucleic acid
          (C)     STRANDEDNESS:   double
          (D)     TOPOLOGY:       linear
     (xi)    SEQUENCE DESCRIPTION: SEQ ID NO:46
CGGCCGCTGC TGCTGCTGTG GCTCTGGGGG CGGCTCCGTG CCCTGACCCA    50
AGGCACTCCG GCGGGGACCG CGCCGACCAA AGACGTGGTG GACTTGGAGT   100
TTTACACCAA GAGGCTATTC CAAAGCGTGA GTCCCTCGTT CCTGTCCATC   150
ACCATCGACG CCAGTCTGGC CACCGACCCT CGGTTCCTCA CCTTCCTGAG   200
CTCTCCACGG CTTCGAGCCC TGTCTAGAGG CTTATCTCCT GCGTACTTGA   250
GATTTGGCGG CACCAAGACT GACTTCCTTA TTTTTGATCC CAACAACGAA   300
CCCACCTCTG AAGAAAGAAG TTACTGGCAA TCTCAAGACA ACAATGATAT   350
TTGCGGGTCT GACCGGGTCT CCGCTGACGT GTTGA                   385
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(2)     INFORMATION FOR SEQ ID NO:47:
          (i)     SEQUENCE CHARACTERISTICS:
                    (A)     LENGTH:         541
                    (B)     TYPE:           nucleic acid
                    (C)     STRANDEDNESS:   double
                    (D)     TOPOLOGY:       linear
          (xi)    SEQUENCE DESCRIPTION: SEQ ID NO:47
AAATCAGGAC ATATCCTTCA CTTATTTGCC TCTTGGTCAT ATTGGAGGCA    50
TTTGTATTCA TTTTTAATAA CCCTCAAAAT AGTGCATGCA AAGTGCTAAG   100
CGTCATTTGC CACATGGTGC CATTAACTGT CACCACCTGC AGTGGTCTAC   150
TTAGAGAACA CCGCACTGGA TGTTAACACT GAAGCGCGTG CCCCGCCCTC   200
CCGAGGCTCT GGATCCAGCG TTGAAGCTTG CCCCGCCCTC CCGAGGCTCT   250
GGATCCAGCA CTGGAGCATG CCCCGCCCTC CCGAGGCTCT GGAGCTTGCT   300
AAGGAGTCCG CTCCCTACCG CTGGGGTTTT GCTTTATTCT TATGAATGAC   350
ACCCCTGACC GCTTTCGTCT CAGGGGTACT GTAATGCCTT TTATTTTCAT   400
ATACAAGCTG CGATTTTGGC ATTTCTTATG ACAAAAAACC CATAGGAAAA   450
GGCGGGCACG CTTAGTGAGC TTCCTGCGGG GAGAGGTTTT TCTGTTAGAG   500
CTGGCANGGT CTGCTCATCG ACCATCTTCA GGCCTCGTGC C            541
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